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IWanaga S., Nishimura H., Kawabata S., Kis
"A new trisaccharide sugar chain linked to
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Zaizov R., Seligsohn U.;
"Ala244Val is a common, probably ancient mudeficiency in Moroccan and Iranian Jews.";
Thromb. Haemost. 76:283-291(1996).
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Alshinawi C., Scerri C., Galdies R.,
"Two new missense mutations (P134T a
                                                                                                                                                                                                                                                  VARIANTS MALTA
                                                                                                                                                                                                                                                                                                            Tamary H., Fromovich Y., Shalmon L.,
Brenner B., Paz M., Luder A.S., Blau
                                                                                                                                                                                                                                                                                                                                                                              deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                          Bernard1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Arbini A.A., Mannucci P.M., Bauer K.A., "A Thr359Met mutation in factor VII of deficiency causes defective secretion o Blood 87:5085-5094(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94264305; PubMed-8204879; Chu K., Friedman Chaing S., Clarke B., Sridhara S., Chu K., Friedman Roberts H.R., Blajchman M., Monroe D.M., High K.A.; "Severe factor VII deficiency caused by mutations ab cleavage site for activation and altering binding to Blood 83:3524-3535(1994).
                                                                                                                                                                                                                                                                                                                                    MEDLINE-97037613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT MIE HIS-307
MEDLINE-95064662; Pt
                                                                                                                                                                                                                                                                                                                                                                                    Bernardí F., Castaman G., Pinotti M.,
Lunghi B., Rodeghiero F., Marchetti G.
"Mutation pattern in clinically asympt
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97001216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Topologically equivalent mutations causing dysfactors VII (294Ala--->Val) and X (334Ser-->Pro) Hum. Mol. Genet. 3:1175-1177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bernardi F., Ca
Rodeghiero F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95072589; PubMed-7981691;
                                 BY A DISULFIDE BOND.

1- ALTERNATIVE PRODUCTS: 2 isoforms; A (s produced by alternative splicing; - TISSUE SPECIFICITY: PLASMA.

1- THE VITAMIN K-DEPENDENT, ENZYMATI GLUTANIC ACID RESIDUES ALLOWS THE MODI CALCIUM.
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   DISEASE: DEFECTS PHARMACEUTICAL: A (Novo Nordisk), U
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talytic domain.
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SUBUNIT: HETERODIMER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                   -325; V-358; Q-3
PubMed-8844208;
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T., Wada H., Minamikawa
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Best Local :
                                                                                                                 FA7_RABIT STANDARD; PRT; 444 AA. P98139; P79224; 01-FEB-1996 (Rel. 33, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
                    <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                              MEDLINE=93190306; PubMed=8383365;
Brothers A.B., Clarke B.J., Sheffield W.P.,
"Complete nucleotide sequence of the cDNA en
factor VII.";
                                                                                                                                                                                                                                                                        TISSUE-Liver;
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     SIMILARITY).

CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-I
form factor xa.

SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND
BY A DISULFIDE BOND (BY SIMILARITY).

TISSUE SPECIFICITY: PLASMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U77477; AAB37326.1; -. P08709; 1FAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ); IPR000152; Asx_hydroxyl.
); IPR001314; Chymotrypsin.
); IPR000561; EGF-11ke.
); IPR000742; EGF_2.
); IPR001881; EGF_Ca.
); IPR002383; GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001254; Ser_protease_Try.
IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease;
sma; Vitamin K; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U179; EGF_CA; 1.

1001; EGF_like; 1.

165; GEA; 1.

20; TYP_SPC; 1.

1010; ASX_HYDROXYL; 1.

122; EGF_1; 1.

136; EGF_2; 1.

15; EGF_2; 1.

16; GLU C^*
                                                                                                                   56
89
94
111
130
137
153
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85
126
192
191
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gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLU_CARBOXYLATION;
TRYPSIN_DOM; 1.
TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN_SER;
       232
281
383
377
100
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141
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191
444
74
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167
1444
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e; Blood coagulation; Zymogen; Glycoprotein;Calcium-binding; Gamma-carboxyglutamic acid
FACTOR IXA, OR THROMBIN) (
BY SIMILARITY.
BY SIMILARITY:
BY SIMILARITY:
BY SIMILARITY:
SUBSTRATE (BY SIMILARITY).
BY SIMILARITY:
BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                            FACTOR VII
FACTOR VII
GLA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                          EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE.
CLEAVAGE (BY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                           1, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S1
                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                      XA,
                                                                                                                                                                                                                                                                                                                                                      FACTOR XIIA
                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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RESULT FAZ-MOUT ID PAZ-MOUT ID
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P70375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-97127167; PubMed-8972017;
Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;

"Nucleotide structure and characterization of the murine blood

"nucleotide structure pane.";

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01-NOV-1997 (Rel. 35
15-JUN-2002 (Rel. 41
Coagulation factor V
                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                               conversion accelerator). F7 OR CF7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVSWGEGCAAVGHVGVYTRVSRYTEWLSRLMRSKLHHGI-QRHPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVPRLMTQDCVEQSEHKPGSPEVTGNMFCAGYLDGSKDACKGDSGG;HATSYHGTWYLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVPRLMTODCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HDIALLRLLQPAALTNNVVPLCLPERNFSESTLATIRFSRVSGWGQLLYRGALARELMAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35, Created)
35, Last sequence update)
41, Last annotation updat
( VII precursor (EC 3.4.21
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71.9%;
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HYDROXYLATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTI
N-LINKED (GLCNAC...) (POTENTI
N-LINKED (GLCNAC...) (POTENTI
N-LINKED (GLCNAC...) (POTENTI
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Pred. No. 2.9e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0481ABC4FE5427F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n update)
3.4.21.21) (Serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
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                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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DOMAIN
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EGF-like
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InterPro;
InterPro;
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InterPro; IPR001254;
InterPro; IPR000294;
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MGD; MGI:109325; F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00134;
PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR00188
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IPR000742;
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FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR A SIMILARITY).
CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile
    AND
A HEAVY CHAIN LINKED
                                                       AND
                           bond
                                                      CALCIUM
                          in
                          factor X to
                                                    (BY
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FORM FACTOR X8.

SUBSINIT: HETERODIMER OF A LIGHT CHAIN AND A BY A DISULFIDE BOND (BY SIMILARITY).

TISSUE SPECIFICITY: PLASMA.

FIM: THE VITAMIN K-DEPENDENT, ENZYMATIC CA.

FORM: THE VITAMIN K-DEPENDENT, ENZYMATIC CA.

FORM: THE WITAMIC ACID RESIDUES ALLOWS THE MODIFIED CALCIUM (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. ENZYMATIC CAF FAMILY S1. CARBOXYLATION IED PROTEIN TO restr and OF SOME for ictions 9 9

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SMARR; SM00020; Tryp_SPC; 1.

PROSITE; PS00010; ASX, HYDROXYL; 1.

PROSITE; PS00022; EGF_1; 1

PROSITE; PS001186; EGF_2; FALSE_NEG.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00111; GLU_CARBOXYLATION; 1

PROSITE; PS000134; TRYPSIN_DOM; 1.

PROSITE; PS000134; TRYPSIN_HIS; 1.

PROSITE; PS000134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0722; CHYMOTRYPSIN PRINTS; PRO0001; GLABLOOD. SWART; SW001079; EGF_CA; 1. SMART; SM00001; EGF_like; 1. SMART; SM00009; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U66079; AAC33796.1; HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                         ase; Serine prote
Plasma; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000152: Asx_hydroxy1.
IPR001314: Chymotrypsin.
                                                                                                                                                                                                                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                      protease;
                                                                                                                                                                                                                                                                                                                                                                        TRYPSIN_SER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF_2.
; EGF_Ca.
; GLA_blood.
; Ser_protease_Try.
vitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                         <u>...</u>
                                                                                                                                                                                                                                                                                                                   Se; Blood coagulation; Zymogen; Glycoprotein;
; Calcium-binding; Gamma-carboxyglutamic acid
Signal; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             like.
FACTOR IXÀ, OR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY:
BY SIMILARITY.
                                                                                                                                                                                          FACTOR VII LIGHT (
FACTOR VII HEAVY (
FACTOR VII HEAVY (
GLA-RICH.
EGE-LIKE 1, CALCII
EGF-LIKE 2
SERINE PROTEASE
                                                                                                                                                                           CLEAVAGE (BY FACTOR
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                             OR THROMBIN)
                                                                                                                                                                                                                        CALCIUM-BINDING
                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                             XA,
                                                                                                                                                                        FACTOR XIIA,
                                                                                                                                                             (BY
                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                           SIMILARITY)
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Best Local S
Matches 275
                                                                                                                                                                                                                                                                                                                                                  _BOVIN
                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                FAI_BOVIN STANDARD; PRT; 407 AA. P22457; 01-AUG-1991 (Rel. 19, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2003 (Rel. 41, Last annotation update) 15-JUN-2004 (Rel. 41, Last annotation update) 15-JUN-2005 (Rel. 41, Last annotation update)
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MOD_RES
        Takeya H.,
                        MEDLINE-89008362; PubMed-3049594;
                                                 SEQUENCE
                                                                                                                                                                                                          accelerator).
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LADGVSCTPTVEYPCGKIPILEKRNASKPQGRIVGGKVCPKGECPWQVLLLVNGAQLCGG
                                                                                                                                                                                                                                                                                                                                                                                                                        HDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPDEVSCKPKVEYPCGRIPVVEKRNSSSRQGRIVGGNVCPKGECPWQAVLKINGLLLCGA
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        Kawabata
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                                                                                                                     Chordata; Craniata; Vertebrata;
Cetartiodactyla; Ruminantia; Per
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68.1%;
    Nakagawa K.,
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GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGL
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Nismatches 82:
    Yamamichi Y.,
                                                                                                                                                                                                                      prothrombin
                                                                                                                       Pecora; Bovoldea;
Miyata
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                                                                                                                                            Euteleostomi;
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THE TERM OF A REAL PROPERTY OF A
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SMART; SM00001; EGF_11ke; 1.

SMART; SM00069; GLA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00020; Tryp_SPG; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00111; GLU_CARBOXYLATION; 1

PROSITE; PS00135; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                        PRINTS; PR00722;
PRINTS; PR00010;
PRINTS; PR00001;
SMART; SM00179;
SMART; SM00001;
                                CHAIN
DOMAIN
                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000152; Asx_hydroxyl InterPro; IPR001314; Chymotrypsin InterPro; IPR000561; EGF-11ke. InterPro; IPR000742; EGF_2. InterPro; IPR001881; EGF_Ca. InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR: A31979; A31979.
HSSP; P08709; 1BF9.
MERODE: A77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hase S., Kawabata S., Nishimura H., Takeya H., Sueyo Miyata T., Iwanaga S., Takao T., Shimonishi Y., Iker "A new trisaccharide sugar chain linked to a serine blood coagulation factors VII and IX.";
J. Blochem. 104:867-868(1988).
                                                                            EGF-like
                                                                                                          Hydrolase;
                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001254;
InterPro; IPR000294;
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91344709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89213999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.";
J. Biol. Chem.
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"Bovine factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: PLASMA.
PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALCIUM.
                                                                                                                                                                                                                                                                                                                                         PE00008; EGF; 2.
PE00089; trypsin; 1.
PE00594; gla; 1.
                                                                                             Plasma;
                                                                                                        Serine protease;
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                                                                                                                                                                                                                                                                                                     22; CHYMOTRYPSIN
10; EGFBLOOD.
01; GLABLOOD.
                                                                                         Vitamin
                                                                                                                                                                                                                                                          EGF_CA; 1.
EGF_like; 1.
GLA; 1.
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 Repeat.
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82.
128
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VitK_dep_GLA.
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                                                                                     calcium-binding; Gamma-carboxyglutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLOWS
FACTOR VII LIGHT OF FACTOR VII HEAVY OF FACTOR VII HEAVY OF GLA-RICH.
EGF-LIKE 1, CALCIL EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYMATIC CARBOXYLATION OF SOME THE MODIFIED PROTEIN TO BIND
            CALCIUM-BINDING
                                           CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sueyoshi
, Ikenaka
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              (POTENTIAL)
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RESULT 5
FA10_CHICK
ID FA10_CHICK
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DT 01-MAY-1992 (
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CARBOHYD
SEQUENCE
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ACT_SITE
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                                                                                   VVSWGEGCAAAGHFGIYTRVSRYTAWLRQLMGHPP
                                                                                                                          CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSL
                                                                                                                                                                  HDVALLQLAQPVALGDHVAPLCLPDPDFADQTLAFVRFSAVSGWGQLLERGVTARKLMVV
                                                                                             IVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEP
                                                                                                                                                                            HDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVL
                                                                                                                                                                                                                                                                                               CEDQLRSYICFCPDGFEGRNCETDKQSQLICANDNGGCEQYCGADPGAGRFCWCHEGYAL
                                                                                                                                                                                                                                                                                                                                                  ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGS
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152
                                  STANDARD;
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   Created)
Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                  SERINE PROTEASE.
CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
FACTOR IXA, OR THROMBIN).
BY SIMILARITY.
B
                                                                                                                                                                                                                                                                                                                                                                                  45;
    sequence
                                                                                                                                                                                                                                                                                                                                                                               Score 1566; DB 1;
Pred. No. 5.7e-115;
5; M1smatches 75;
                                  PRT;
   update
                                 475
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                                                                                    395
                                                                                                                                                                                                                                                                                                                                                                                                   Length 407;
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 WEROPS; SO1.116; ...
InterPro: IPR0001514; Chym
InterPro: IPR0001314; Chym
InterPro: IPR0001561; EGF-
InterPro: IPR000742; EGF-
InterPro: IPR001388; EGF-
InterPro: IPR001388; EGF-
InterPro: IPR002383; GLA_
InterPro: IPR002383; GLA_
InterPro: IPR001554; Ser_
InterPro: IPR000294; VitR
Pfam; PF00008; EGF; 2.
Pfam; PF00008; Trypsin; 1
Pfam; PF00089; Trypsin; 1
Pfam; PF00089; Jak; 1.
                                                                                                                                             EMBL; D00844;
PIR; S15838; S
HSSP; P00742;
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Ogasawara T.,
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: PF00594; gl
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FX.
Gallus gallus (Chicke Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determinant of viral tropism in chick embryo.";
EMBO J. 9:4189-4195(1990).

-I FUNCTION: Factor xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-I FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV, AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLAN.
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MEDLINE-91257322; PubMed-2044767;
Suzuki H., Harada A., Hayashi Y.,
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"An endoprotease homologous to
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SINCE Allantoic fluid;
MEDLINE-91065352; PubMed-2174359;
MEDLINE-91065352; PubMed-2174359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Primary structure of the virus activating protease embryo. Its identity with the blood clotting factor FEBS Lett. 283:281-285(1991).
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Coagulation factor
(Virus activating p
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IN TISSUE SPECIFICITY: LIVER AND CHORIOALLANT

PITM: THE VITAMIN K-DEPENDENT, ENZYMATIC CA
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED
CALCIUM.

CALCIUM.

PITM: THE ACTIVATION PEPTIDE IS CLEAVED BY
INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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CARALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
HE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
IC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                             S15838.
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tazoa; Chordata;
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X precursor (EC 3.4.21.6) (Stuart factor)
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Chymotrypsin.
EGF-like.
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domain; Repeat.
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roxylation; Calcium-binding; Vitamin
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TISSUE-Liver;
MEDLINE-86221713; PubMed-3011603;
Kaul R.K., Hildebrand B., Roberts
"Isolation and characterization o
                                                                                                                                        SEQUENCE OF 13-488 FROM N.A.

MEDLINE-85216545; PubMed-2582420;
Fung M.R., Hay C.W., McGillivray R.T.A.;

"Characterization of an almost full-length cDNA coding blood coagulation factor X.";

Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
                                                                                                                                                                                                                                                                                                                                            MEDIINE-87026600; PubMed-3768336;
Leytus S.P., Foster D.C., Kurachi K., Davie E.W.,
"Gene for human factor X: a blood coagulation factor whose
organization is essentially identical with that of factor I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA10_HUMAN STANDARD; PRT; 488 AA.
P00742; Q14340;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Messler T.L., Pittman D.D., Long "Cloning and expression in COS-1 human coagulation factor X."; Gene 99:291-294(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-91216473; Pub)
Messier T.L., Pittman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278. MEDLINE-93360277; PubMed-8355279; MEDLINE-93360277; PubMed-8355279; Padmanabhan K.P., Tulinsky A., Park C.H., Bode Padmanabhan K.P., Tulinsky A., Park C.H., Bode Huber R., Blankenship D.T., Cardin A.D., Kisiel W.; "Structure of human des(1-45) factor Xa at 2.2-A resolution."; J., Mol. Biol. 232:947-966(1993).
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Eur. J. Biochem. 218:153-163(1993).
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Biochemistry 22:2875-2884(1983).
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                                                                                                                                                                                                                                                                                                       FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood coletting. CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin. SUBGUIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OF
                                                                                                                                                        INTRINSIC PATHWAY), C
SIMILARITY: BELONGS T
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Plasma; synthesized in the liver. PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATICN OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
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of human blood coagulation
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JR SMART; SM00000; Tryp_SPC; 1.
PROSITE: PS00010; ASX, HYDROXYL; 1.
DR PROSITE: PS0001186; EGF_C; 2.
DR PROSITE: PS001187; EGF_CA; 1.
DR PROSITE: PS001187; EGF_CA; 1.
DR PROSITE: PS001187; EGF_CA; 1.
DR PROSITE: PS00134; TRYPSIN_DOM; 1.
DR PROSITE: PS000134; TRYPSIN_HHS; 1.
PROSITE: PS00134; TRYPSIN_SER; 1.
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PROSITE: PS00135; TRYPSIN_SER; 1.
PROSITE: PS00136; TRYPSIN_SER; 1.
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P00741;
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Katayama K., Ericsson L.H., Enfield
Davie E.W., Titani K.;
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                                                                                                                                                                                                                                                                                       KLSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSMGEGCARK
                                                                                                                                                                                        STANDARD;
                                                                                                                                   1,44
1,44
1,44
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322
419
101
110
121
140
                                                                                    Chordata; Craniata; Vertebrata; Eute: Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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103
199
211
221
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Last sequence update)
Last annotation update)
(EC 3.4.21.22) (Christmas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-CARBOXYGLUTAMIC ACID.
HYDROXYLATION.
O-LINKED (GALNAC. .),
O-LINKED (GALNAC. .),
N-LINKED (GLONAC. .),
/FTIG-CAR_O00012.
N-LINKED (GLONAC. .),
/FTIG-CAR_000013.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 858.5; DB 1;
Pred. No. 9.5e-60;
6; Mismatches 146;
 of.
                    D.L.,
                                                                                                                                                                                       416
bovine
                                                                                                                                                                                       Å
                     Walsh
                                                                                                                                                                                                                                                                  404
coagulation
                                                                                                                                factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                               Euteleostomi;
                     Neurath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
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InterPro; IPR000152; A
InterPro; IPR001314; C
InterPro; IPR000561; E
InterPro; IPR000742; E
InterPro; IPR001861; E
                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 This SWI
                                                                                            MEROPS; S01.214; -. GlycoSuiteDB; P00741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE OF CARBOHYDRATE ON SER-53.

MEDLIXE-91344709; PubMed-2129367;

IWANAGA S., Nishimura H., Kawabata S., Kisiel W., Hase S., I
"A new trisaccharide sugar chain linked to a serine residue
first EGF-like domain of clotting factors VII and IX and pro
Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                                                           PIR; A00923; KFBO
HSSP; P00740; 1CFI
                                                                                                                                                           EMBL; J00007; AAA30520.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE OF CARBOHYDRATE ON SER-53.

MEDLINE-89213999; PubMed-3149637;

Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,

Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;

"A new trisaccharide sugar chain linked to a serine residue blood coagulation factors VII and IX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-82272386; PubMed-628728
Choo K.H., Gould K.G., Rees D.J
"Molecular cloning of the gene
Nature 299:178-180(1982).
                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE OF CARBOHYDRATE ON SER-53.
MEDLINE-90130422; PubMed-2105311;
Hase S., Nishimura H., Kawabata S., Iwanaga
"The structure of (xylose)2glucose-0-serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMullen B.A., Fujikawa K., Kisiel W.;
"The occurrence of beta-hydroxyaspartic
K-dependent blood coagulation zymogens."
Biochem. Biophys. Res. Commun. 115:8-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE OF CARBOHYDRATE ON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83308813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Christmas Factor) with that of other vitamin K-dependent plasma proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem, 104:867-868(1988).
                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no restroy non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO SIMILARITY: CONTAINS 2
                                                                                                                                                                                                                                                                                                                                         FORM FACTOR XA.

SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONGS.

MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 265:1858-1861(1990).

FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.

CATALYTIC ACTIVITY: Hydrolyzes one Arg-I-ile bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 51-111 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth factor-like
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                                                                                                                            1CFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation zymogens.";
Res. Commun. 115:8-14(1983)
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Chymotrypsin.
EGF-11ke.
EGF_2.
EGF_Ca.
EGF_II.
                                                                            Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A. 76:4990-4994(1979)
                                                                                                                                                                                                                                                                                                              PEPTIDASE FAMILY S1. EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
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human anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anaga S., Ikenaka
erine 53 found in
bovine blood clot
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anti-haemophilic
                                                                                                                                                                                                                   Usage
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ie in the
protein Z.";
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of factor
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Matches 167
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PROSITE;
PROSITE;
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SMART; SM00179; 1
SMART; SM00001; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PFNNTS; PR00722; CHYMOTRYP;
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002383; InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lood coagulation;
             71
                                                                                              il Similarity
167; Conser
                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00020; Tryp_SPc; 1.
E; PS00010; ASX_HYDRXYL; 1
E; PS00022; EGF_1; 1
E; PS01186; EGF_2; 2.
E; PS01187; EGF_CA; 1.
    FCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPT
                             GNLERECKEEKCSFEEAREVFENTEKTTEFWKQYVDGDQCESNPCLNGGMCKDDINSYEC
                                                        GSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYIC
                                                                                                                                                    158
168
173
261
222
270
366
64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ulation; Plasma; Serine protease; Calcium-binding; Glycoprotein; Vitamin K; Gamma-carboxyglutamic acid; Hydroxyjation; Zymogen; EGF-Like domain.

1 146 FACTOR IXA (ACTIVE FORM) LIGHT CHA
                                                                                            Conservative
                                                                                                                                                                                                                                                                                           EGF_CA; 1.
; EGF_like; 1.
; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF; 2.
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TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLU_CARBOXYLATION;
TRYPSIN_DOM; 1.
                                                                                                                                                               158
168
173
261
222
270
366
                                                                                                                                                                                                                                                                                           82
99
109
124
                                                                                                                                                    46785
                                                                                                        38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLA_blood:
Ser_protease_Try.
V1tK_dep_GLA:
                                                                                                                                                  MW;
                                                                                                                                                        HYDROXYLATION.
BY SIMILARITY
CHINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE (BY FACTOR XIA).
CLEAVAGE (BY FACTOR XIA).
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                        Score 850.5;
Pred. No. 3,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE 1, CALCIUM-BINDING EGF-LIKE 2.
                                                                                                                                              34A7DFE916330662 CRC64;
                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEASE
                                                                                                        .4e-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ACTIVE FORM) HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ACTIVE FORM) LIGHT CHAIN
                                                                                                                    DB 1;
                                                                                       Indels
                                                                                                                 Length
                                                                                                                 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                       51;
                                                                                     Gaps
                              71
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ID _HUMAN

ID _HOMAN

ID _HOMAN

ID _HOMO

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  Jagadeeswaran
              MEDLINE-84300526;
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FA9_HUMAN STANDARD.

FA9_HUMAN STANDARD.

P00740:
21-JUL-1986 (Rel. 01, Created)
01-JAN.1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Dast annotation update)
                                                                                                           Jaye M., de la Salle H., Schamber F., Bal Findell A., Tolstoshev P., Lecocq J.P.; "Isolation of a human anti-heemophilic fa unique 52-base synthetic oligonucleotide acid sequence of bovine factor IX.; Nucleic Acids Res. 11:2325-2335(1983).
                                                                                                                                                                                                                                                                                                         MEDLINE=84236100; PubMed=6329734;
Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.o
Huddleston J.A., Brownlee G.G.;
"The gene structure of human anti-haemophilic factor IX.";
EMBO J. 3:1053-1060(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.I Graham J.B., Stafford D.W., "Bytdence for a prevalent dimorphism in the activ human coagulation factor IX.", Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-83220788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 24:3736-3750(1985).
                                                                       EQUENCE OF 36-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-65000558; Pubmed=2994716;
YOShitake S., Schach B.G., Foster D.C.,
"Nucleotide sequence of the gene for hur
factor B).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=85190593; PubMed=3857619;
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Cell 82:131-141(1995).
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PRINTS; PRODOO1; GLABLOUD.

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SMART; SM00019; EGF_11ke; 1.

SMART; SM00001; EGF_11ke; 1.

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PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00012; EGF_1; 1.

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PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00111; GLU_CARBOXYLATION; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1. InterPro; IPR002383; GLA_blood.
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InterPro; IPR000294; V1tK_dep_GLA. lycoprotein; Hydrolase; Serine amma-carboxyglutamic acid; Hydr IPRO00152: Asx_hydroxyl.
IPRO01314: Chymotrypsin.
IPR000561: EGF-11ke.
IPR000742: EGF_2. ; trypsin; 1. ; gla; 1. AAB62542.1; -. 20 180 190 232 232 165 165 like Serine protease; id; Hydroxylation; domain; Repeat. GAMMA-CARBOXYGLUTAMIC FACTOR X LIGHT CHAIN.
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MEDLINE-84185716; PubMed-6546930; Sugo T., Bjoerk I., Holmgren A., Stenflo J.; "Calcium-binding properties of bovine factor carboxyglutamic acid-containing region."; J. Biol. Chem. 259:5705-5710(1984).
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                                                                                                                                                                                                                                              MEDLINE-76053121; pubMed-1059122;
Fujikawa K., Titani K., Davie E.W.;
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Indue K., Morita T.;
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K-dependent blood coagulation zymogens"
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MEDLINE-94062825; Pul
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MEDLINE-83308813;
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MEDLINE=80130563; PubMed=6766735;
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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the activation of factor
schem. 218:153-163(1993).
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             261:4008-4014(1986).
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son M.A., Fujikawa
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PubMed=8243461;
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                                     difference between bovine blood o tyrosine 18 in the activation
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Trewhella J.;
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Sunnerhagen M., Olah
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STRUCTURE BY NMR OF 85-126.
MEDLING-92406922; PubMed-1527084;
MEDLING-92406928; Vullner M.,
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                              GlycoSuiteDB;
InterPro; IPR
                                                                                                                EMBL; X00673; CAA25286.1;
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J. Biol. Chem. 267:19642-19649(1992).
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MEDLINE-92329412: PubMed-1627540;
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MEDLINE-91084483; PubMed-2261466;
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; 1CCF; 31-MAY-94.
; 1WHE; 15-MAY-97.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

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PTM: THE VITAMIN K-DEPENDENT,
GLUTAMIC ACID RESIDUES ALLOWS
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        eDB; P00743; -.
IPR000152; Asx_hydroxyl.
IPR001314; Chymotrypsin.
IPR000561; EGF-11ke.
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SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS001186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001187; EGF_CA; 1.

PROSITE; PS00011; TRYPSIN_DOM; 1.

PROSITE; PS00014; TRYPSIN_HIS; 1.

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256 DHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSR : | | | | | | | : : | : | : | : | | : | | : | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE 1, CALCIUM-BIN
EGF-LIKE 2,
SERIME PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA. H.
MAY BE REMOVED BUT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 843; DB 1;
Pred. No. 1.6e-58;
0; Mismatches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION.
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    CALCIUM-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 492,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
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8 8 8

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MGD; MGI:88384; F9:
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2:
InterPro; IPR001181; EGF_Ca.
InterPro; IPR001254; Ser_protease_T;
InterPro; IPR001254; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                          Sarkar G., Koeberl D.D., Sommer S.S.;

**Plirect sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species.**;

Genomics 6:133-143(1990).

-i- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PACHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++

IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.

-i- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FA9_MOUSE
P16294;
01-AUG-1990
01-FEB-1991
15-JUN-2002
                                                                                                                                                        EMBL; M23109; AAA37629.1;
EMBL; M26236; AAA37630.1;
PIR; JQ0419; JQ0419.
HSSP; P00740; 1CFH.
                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                           MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-90215309; PubMed-2323576; MEDLINE-90215309; PubMed-2323576; Mare J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 168-451 FROM N.A. MEDLINE-90152675; PubMed-2303254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 86:275-278(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
F9 OR CF9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu S.-M., Stafford D.W., ware J., "Deduced amino acid sequence of mouse blood-coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                      form factor Xa.

SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PERTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR DISULFIDE BONDS.
 PF00008; EGF; 2.
PF00089; trypsin; 1.
PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 VYTRVSQYIEWLQKLMRS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390
                                                                                                                                          S01.214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYTKVSNFLKWIDKIMKA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLSSSTITPNMFCAGYDTQPEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKFG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGGGCATVGHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNVAPACLPEKDWAEATLMTQKTGIVSGFGRTHEKGRLSSTLKMLEVPYVDRSTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 15, Created)
(Rel. 17, Last sequence (Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                        Ser_protease_Try.
_VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
precursor (EC 3.4.21.22) (Christmas factor)
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ş
                                                                              Query Match
Best Local s
Matches 169
                                                                                          CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                            DISULFID
DISULFID
DISULFID
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DISULFID
DISULFID
                                                                              SEQUENCE
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CHAIN
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DOMAIN
                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                            ACT_SITE
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NON_TER
SIGNAL
                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00179;
SMART; SM00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
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211
304
363
388
459
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265
313
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DA A CONSTRUCTION OF THE TRANSPORT OF TH

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SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS0011; GLU_CARBOXYLATION; 1.

PROSITE; PS00104; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blood coagulation; Plasma; Serine protease; Calcium-binding; Hydrolase; Glycoprotein; Vitamin K; Gamma-carboxyglutamic ac Hemophilia; Hydroxylation; Zymogen; Signal; EGF-like domain;
                     Similarity
    Conservative
                                                                   AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_CA; 1.
                                                                                105
116
133
143
158
158
192
211
304
363
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180
180
180
189
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117
117
1189
                                                                   51635 MW;
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                   37.78;
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    57;
                                                                                                        BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
 Score 824; DB 1;
Pred No. 4.4e-57;
7; Mismatches 132
                                                                                H -> Q (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE.
CLEAVAGE (BY FACTOR XIA) (I
CLEAVAGE (BY FACTOR XIA) (I
CLEAVAGE (BY FACTOR XIA) (I
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR IXA (ACTIVE FORM) LIGHT ACTIVATION PEPTIDE.
FACTOR IXA (ACTIVE FORM) HEAVY EGF-LIKE 1, CALCIUM-BINDING (PC EGF-LIKE 2).
                                                                                                                                                                                                                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                    GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                     HYDROXYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                   GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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                                                              EF439C840D6CBClA CRC64;
                             Length 459;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACID
                                                                                                          (POTENTIAL)
(POTENTIAL)
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(POTENTIAL).
 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
Gaps
 10;
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105

THE

collaboration -

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01-FEB-1991
01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                          MEDLINE-89323338; PubMed-2752110;
Evans J.P., Watzke H.H., Ware J.L., Stafford
"Molecular cloning of a cDNA encoding canine
Blood 74:207-212(1989).
                                                                                                                                                                                                                                                                                                                        MEDLINE=90311364; PubMed=2367529;
Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.;
Phenotypic correction of factor IX deficiency in sk
hemophilic dogs.";
Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FA9_CANFA
P19540;
                                                                                                                    consequences.
                                                                                                                       MEDIINE-90099303; PubMed-2481310;
Evans J.P., Brinkhous K.M., Brayer G.D., Reisner H.M., Hi
"Canine hemophilia B resulting from a point mutation with
consequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coagulation
                                                                                                                                                                                 VARIANT HEMOPHILIA B GLU-418
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SSUE-Liver;
             CHALL ACAD. SCI. U.S.A. 86:10095-10099(1989).

EUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PARTMAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385
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         factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFTTYNNMFCAGYREGGKDSCEGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTK 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSRYVNWIKE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSQYIEWLQK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NITEY--MFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANR---EYTNIFLKFGSGYVSGWGKVFNKGRHASILQYLRVPLVDKATCLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAGEYNIDKKEDTEGRRNVIRT-IPHHQYNATINKYSHDIALLELDKPLILNSYVTPICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTN---HDIALLRLHQPVVLTDHVVPLCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVGAAHCF---DKIKNWRNLIA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPFPCGRASISYSSKKITRAETVFSNMDYENSTEAVFIQDDITDGAILNNVTESSESLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 17, Created)
  (Rel. 17, Last sequence update)
  (Rel. 41, Last annotation update)
  factor IX precursor (EC 3.4.21.22) (Christmas factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                   87:5173-5177(1990).
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                                                                                                                                                                                                                          D.W., High K.A.; factor IX.";
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PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0701; GLABLOOD.
SMART; SMO0179; EGF_CA; 1.
SMART; SM00079; GLA; 1.
SMART; SM00009; TIYP_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00118; EGF_C1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00114; GLU_CARBOXYLATION; 1.
PROSITE; PS00135; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                Repeat;
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                                          MOD_RES
                                                                        MOD_RES
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                      MOD_RES
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      Blood coagulation; Plasma; Serine Hydrolase; Glycoprotein; Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                      MOD_RES
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InterPro;
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EMBL; M33826; AAA30844.1; --
PIR; A30351; A30351.
HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                                                                                                              Hemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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InterPro; IPR000294;
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MEROPS;
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InterPro: IPR001881;
InterPro: IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000152; Asx_hydroxyl
InterPro: IPR001314; Chymotrypsin
InterPro: IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES TH ACTIVATION PERTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MONE DISULTIDE BONDS.

DISEASE: HEMOCHILIA B IS DUE TO DEFECTS IN FACTOR IX MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.

BEYOND THE GLA DOMAIN 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00089; trypsin; 1.
PF00594; gla; 1.
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                                                                                                                                                                                                                                                                                                                                               Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S01.214;
                                                                                                                                                                                                                                                                                                                                                       Hydroxylation;
                                              59
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                                                                                                                                                                                                                                                                                                                                             mutation
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217
452
122
164
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V1tK_dep_GLA.
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                                                                                                                                                                                                                                                                                                                                                                      Serine protease; Calcium-binding; itamin K; Gamma-carboxyglutamic ac
                                                      GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY)
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY)
GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                         Zymogen;
                        GAMMA-CARBOXYGLUTAMIC (BY SIMILARITY).
                                                                                                                                                             CLEAVAGE (BY FACTOR XIA) (BY CLEAVAGE (BY FACTOR XIA) (BY GAMMA-CARBOXGLUTAMIC ACID
                                                                                                                                                                                                                          FACTOR IXA (ACTIVE FORM) LIGHT CHAIN ACTIVATION PEPTIDE.
FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTI)
EGF-LIKE 2.
        GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                 CLEAVAGE (BY FACTOR CLEAVAGE (BY FACTOR
                                                                                                                                                                                                                  SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                         Signal;
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        ACID
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Best Local S
Matches 163
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CARBOHYD
ACT_SITE
ACT_SITE
ACT_SITE
VARIANT
                                 PRTC_PIG STANDARD; PRT; 459 AA 09GLP2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update Vitamin-K dependent protein C precursor (EC (Autoprothrombin IIA) (Anticoagulant protei
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                  actor XIV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFD-KIKNWRNLIAVLGEHDLSEHDGDE
                                                                                                                                                                                                                               KDSCQGDSGGPHYTEVEGISFLTGIISWGEECAMKGKYGIYTKVSRYVNWIKE
                                                                                                                                                                                                                                                               KDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQK
                                                                                                                                                                                                                                                                                                     GSGYVSGWGRVFNKGRSASILQYLKVPLVDRATCLRSTKF----TIYNNMFCAGFHEGG
                                                                                                                                                                                                                                                                                                                                     --SLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGS
                                                                                                                                                                                                                                                                                                                                                                          QKRNVIRTILHHSYNATINKYNHDIALLELDEPLTLNSYVTPICIADREYSN---IFLKF
                                                                                                                                                                                                                                                                                                                                                                                               QSRRVAQVIIPSTY--VPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTESEETLAFVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FCLPAFEGRNCETHKDDQLICVNENGGCEQVCSDHTGTKRSCRCHEGYSLLADGVSCTPT
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39.5%;
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                          rotein C precursor (EC 3. (Anticoagulant protein C
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
G -> E (IN HEMOPHILIA B).
W: 1F6537C46A6960ED CRC64;
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BY
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Pred. No. 7.4e-57;
7; Mismatches 133
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BY SIMILARITY
BY SIMILARITY
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GAMMA-CARBOXYGLUTAMIC
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                              3.4.21.69)
C) (Blood
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                              coagulation
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R PRINTS; PRO072; CLABLOOD.
R PRINTS; PRO072; CLABLOOD.
SMART; SM000181; EGF; 2.
SMART; SM00001; EGF_11ke; 2.
SMART; SM00069: CT.

SMART; SM00069; GLA; 1
SMART; SM00020; Tryp_SPC; 1
SMART; SM00020; Tryp_SPC; 1
PROSITE; PS00010; ASX_HYDRXYL; 1.
PROSITE; PS00022; EGE 1; 1
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; GLU_CARBOXYLATION; 1
PROSITE; PS00011; GLU_CARBOXYLATION; 1
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESR; 1.

Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.

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InterPro; IPR000152; InterPro; IPR001314; InterPro; IPR000561; InterPro; IPR001881; InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -is SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-in TISSUE SPECIFICITY: Plasma; Synthesized in the liver.
-in PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-in MISCELLANDOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
-in SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-in SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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Mammalia; Eutheria; (
NCBI_TaxID=9823;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grimm D.R., Colter M.B., Braunschw. Kim H.K.W.;
                                                                                                                                                                                                                                                                                                           Pfam;
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1- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

1- SUBUNIT: Synthesized as a single chain precursor, which is cleave.
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InterPro; IPR001254;
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PF00089; trypsin; 1.
PF00594; gla; 1.
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
"The cDNA cloning and mRNA expression of rat protein C.";
Biochim. Biophys. Acta 1131:329-332(1992).
-i- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-i- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.
(Autoprothrombin IIA) (Anticoagulant protein C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Liver; MEDLINE-92329550; PubMed-1627650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                               STRONGLY PROMOTED BY THROMBOMODULIN.

TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

PIM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXLATION OF S
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBOMODULIN COMPLEX.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND VIIIA.
SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461
                                      noved. Usage by and for (See http://www.isb-sib
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                                                                                                                     restrictions
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Asx_hydroxyl..

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SMART; SM00020; TTYP_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS001186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001187; EGF_CA; 1.

PROSITE; PS00011; GLU_CARBOXYLATION

PROSITE; PS000134; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
      ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
CARBOHYD
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PEPTIDE
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Interpro;
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SM00001;
SM00069;
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IPR001254; Ser_protease_Try.
IPR000294; V1tK_dep_GLA.
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EGF_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tamic acid; Calcium-binding; Vitamin |
Repeat; Endotheilal cell; Hydrolase;
32 By SIMTLADITY
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                              ; Chymotrypsin.
; EGF-11ke.
; EGF_Ca.
           51912
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           Ĭ.
HYDROXYLATION (BY SIMILARITY)
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY 
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PROTEIN C HEAVY CHAIN (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

CLEAVAGE (BY THROMBIN) (BY SIMILARITY).

EGF-LIKE 1.
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PROPERTY AND THE PROPER
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PRTC_MOUSE
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Best Local
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PRTC_MOUSE STAND:
P33587; 035498;
01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
15-JUN-2002 (Rel. 41,
Vitamin-K dependent p
(Autoprothrombin IIA)
                                                                                                       STRAIN-129/SvJ;
MEDLINE-98152576; PubMed-9493582;
                                                                                                                                                                              TISSUE-Liver;

MEDLINE-92316897; PubMed-1618739;

Tada N., Sato M., Tsujimura A., Iwase R.,

"Isolation and characterization of a moust
J. Biochem. 111:491-495(1992).
STRAIN=BALB/c;
MEDLINE=94318474; PubMed=8043441;
                                                           "Nucleotide structure anticoagulant protein Thromb. Haemost. 79:31
                                                                                                    Jalbert L.R., Ro
Castellino F.J.;
                              SEQUENCE OF 274-434
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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AGIIGDTRDACDGDSGGPMVVFFRGTWFLVGLVSWGEGCGHLNNYGVYTKVGSYLKWIHS
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. 28, Last sequence update)
. 41, Last annotation update)
lent protein C precursor (EC 3)
IIA) (Anticoagulant protein
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Murinae; Mus
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PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0701; GLABLOOD.
SMARR; SM0010; EGF_ILKe; 1.
SMARR; SM0000; EGF_IKe; 1.
SMARR; SM0000; Tryp_SPC; 1.
SMARR; SM00000; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01186; EGF_Z; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00113; TRYPSIN_DOM; 1.
PROSITE; PS0013; TRYPSIN_HIS; 1.
PROSITE; PS0013; TRYPSIN_HIS; 1.
PROSITE; PS0013; TRYPSIN_HIS; 1.
PROSITE; PS0013; TRYPSIN_HIS; 1.
PROSITE; PS0013; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxy1.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR0012383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; V1tK_dep_GLA.
              SIGNAL
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CHAIN
PEPTIDE
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Pfam; PF00089; tryp;
Pfam; PF00594; gla;
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                                                                                    Blood coagulation; Gly
Gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.218; -. MGD; MGI:97771; Proc.
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EMBL; AF034569; AAC33795.1
EMBL; D43755; BAA07812.1;
PIR; JX0210; JX0210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Romparative study of partial primary structures of the region of mammalian protein C.";

Br. J. Haematol. 86:590-600(1994).

-i- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS.

IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-i- CATALYTIC ACTIVITY: Degradation of blood coagulation
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                                                                          Repeat;
                                                                     Glycoprotein; Serine protease;
mic acid; Calcium-binding; Vitamin ;
epeat; Endothelial cell; Hydrolase;
                PROTEIN C LIGHT CHAIN (
PROTEIN C HEAVY CHAIN (
ACTIVATION PEPTIDE (BY
           CLEAVAGE (BY THROMBIN)
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BY SIMILARITY.
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SDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMR
                 TVVTGWGYOSDRIKDGRRNRTFI-LTFIRIPLVARNECVEVMKNV--
                                                                                                                     KGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGD
                                                                                                                                                              RCHEGYSLLADGVSCTPTVEYPCGKIP--ILEKRNASK------
                                     SLVSGWGQLLD-----RGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGY
                                                             ELDLDIKEILVHPNYTRSSSDNDIALLRLAQPATLSKTIVPICLPNNGLAQQELTQAGQE
                                                                                 EQSRRVAQVIIPSTYVPGTTNHDIÄLLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RF
                                                                                                      QGDSPWQAILLDSKKKLACGGVLIHTSWVLTAAHC---VEGTKKLTVRLGEYDLRRRDHW
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